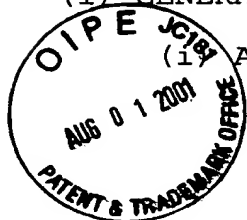


SEQUENCE LISTING

(1) GENERAL INFORMATION:



(i) APPLICANT: PAUL, PREM S.  
MENG, XIANG-JIN  
HALBUR, PATRICK G.  
MOROZOV, IGOR  
LUM, MELISSA A.

#6

(ii) TITLE OF INVENTION: A POLYNUCLEIC ACID ISOLATED FROM A PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR PROTEIN,

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, P.C.  
(B) STREET: 1755 S. Jefferson Davis Highway, Suite 400  
(C) CITY: Arlington  
(D) STATE: Virginia  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22202

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/131,625  
(B) FILING DATE: 05-OCT-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lavalleye, Jean-Paul M.P.  
(B) REGISTRATION NUMBER: 31,451  
(C) REFERENCE/DOCKET NUMBER: 4625-021-55X CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 413-3000  
(B) TELEFAX: (703) 413-2220  
(C) TELEX: 248855 OPAT UR

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCCGTGTG GTTCTCGCCA AT

22

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCATTTCC CTCTAGCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGCGGAAC CATCAAGCAC

20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAACTTGACG CTATGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGTCTGGA TTGACGACAG

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTGCTAGG GCTTCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCATTCAGC TCACATAGCG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCGTCAAGT ATGGCCGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCATTCGCC TGACTGTCA

19

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGACGAGGA CTTCGGCTG

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTCTACCTG CAATTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGTATAGGA CCGGCAACCG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCAGGCTTT GCTGTCCTCC AAGACATCAG TTGCCTTAGG CATCGCAACT CGGCCTCTGA	60
GGCGATTTCGC AAAGTCCCTC AGTGCCGCAC GGCGATAGGG ACACCCGTGT ATATCACTGT	120
CACAGCCAAT GTTACCGATG AGAATTATTT GCATTCTCTCT GATCTTCTCA TGCTTTCTTC	180
TTGCCTTTTC TATGCTTCTG AGATGAGTGA AAAGGGATTT AAGGTGGTAT TTGGCAATGT	240
GTCAGGCATC GTGGCAGTGT GCGTCAACTT CACCAGTTAC GTCCAACATG TCAAGGAATT	300
TACCCAACGT TCCTTGGTAG TTGACCATGT GCGGCTGCTC CATTTCATGA CGCCCGAGAC	360
CATGAGGTGG GCAACTGTTT TAGCCTGTCT TTTTGGCATT CTGTTGGCAA TTTGAATGTT	420
TAAGTATGTT GGGGAAATGC TTGACCGCGG GCTGTTGCTC GCAATTGCTT TTTTGTGGT	480
GTATCGTGCC GTCTTGTTTT GTTGCGCTCG TCAGCGCCAA CGGGAACAGC GGCTCAAATT	540
TACAGCTGAT TTACAACTTG ACGCTATGTG AGCTGAATGG CACAGATTGG CTAGCTAATA	600
AATTTGACTG GGCAGTGGAG TGTTTTGTCA TTTTTCCTGT GTTGACTCAC ATTGTCTCTT	660
ATGGTGCCCT CACTACTAGC CATTTCTTG ACACAGTCGG TCTGGTCACT GTGTCTACCG	720
CTGGGTTTGT TCACGGGCGG TATGTTCTGA GTAGCATGTA CGCGGTCTGT GCCCTGGCTG	780
CGTTGATTTG CTTTCGTCATT AGGCTTGCGA AGAATTGCAT GTCCTGGCGC TACTCATGTA	840
CCAGATATAC CAACTTTCTT CTGGACACTA AGGGCAGACT CTATCGTTGG CGGTCGCCTG	900
TCATCATAGA GAAAAGGGGC AAAGTTGAGG TCGAAGGTCA CCTGATCGAC CTCAAAGAG	960
TTGTGCTTGA TGGTTCCGCG GCTACCCCTG TAACCAGAGT TTCAGCGGAA CAATGGAGTC	1020
GTCCTTAGAT GACTTCTGTC ATGATAGCAC GGCTCCACAA AAGGTGCTCT TGGCGTTTTC	1080
TATTACCTAC ACGCCAGTGA TGATATATGC CCTAAAGGTG AGTCGCGGCC GACTGCTAGG	1140
GCTTCTGCAC CTTTTGGTCT TCCTGAATTG TGCTTTCACC TTCGGGTACA TGACATTCGT	1200
GCACTTTCAG AGTACAAATA AGGTCGCGCT CACTATGGGA GCAGTAGTTG CACTCCTTTG	1260
GGGGGTGTAC TCAGCCATAG AAACCTGGAA ATTCATCACC TCCAGATGCC GTTTGTGCTT	1320

GCTAGGCCGC	AAGTACATTC	TGGCCCCCTGC	CCACCACGTT	GAAAGTGCCG	CAGGCTTTCA	1380
TCCGATTGCG	GCAAAATGATA	ACCACGCATT	TGTCGTCCGG	CGTCCCGGCT	CCACTACGGT	1440
CAACGGCACA	TTGGTGCCCG	GGTTAAAAAG	CCTCGTGTTG	GGTGGCAGAA	AAGCTGTTAA	1500
ACAGGGAGTG	GTAAACCTTG	TTAAATATGC	CAAATAACAC	CGGCAAGCAG	CAGAAGAGAA	1560
AGAAGGGGGA	TGGCCAGCCA	GTCAATCAGC	TGTGCCAGAT	GCTGGGTAAG	ATCATCGCTC	1620
ACCAAAACCA	GTCCAGAGGC	AAGGGACCGG	GAAAGAAAAA	TAAGAAGAAA	AACCCGGAGA	1680
AGCCCCATTT	CCCTCTAGCG	ACTGAAGATG	ATGTCAGACA	TCACTTTACC	CCTAGTGAGC	1740
GTCAATTGTG	TCTGTCGTCA	ATCCAGACCG	CCTTTAATCA	AGGCGCTGGG	ACTTGCACCC	1800
TGTCAGATTC	AGGGAGGATA	AGTTACACTG	TGGAGTTTAG	TTTGCCTACG	CATCATACTG	1860
TGCGCCTGAT	CCGCGTCACA	GCATCACCCT	CAGCATGATG	GGCTGGCATT	CTTGAGGCAT	1920
CCCAGTGTTT	GAATTGGAAG	AATGCGTGGT	GAATGGCACT	GATTGACATT	GTGCCTCTAA	1980
GTCACCTATT	CAATTAGGGC	GACCGTGTGG	GGGTAAGATT	TAATTGGCGA	GAACCACACG	2040
GCCGAAATTA	AAAAAAAAAA	AA				2062

(2) INFORMATION FOR SEO ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus  
(B) STRAIN: Iowa  
(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG TTG GGG AAA TGC TTG ACC GCG GGC TGT TGC TCG CAA TTG CTT TTT 48  
Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe  
1 5 10 15

[illegible]



(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Leu	Gly	Lys	Cys	Leu	Thr	Ala	Gly	Cys	Cys	Ser	Gln	Leu	Leu	Phe	1	5	10	15
Leu	Trp	Cys	Ile	Val	Pro	Ser	Cys	Phe	Val	Ala	Leu	Val	Ser	Ala	Asn	20	25	30	
Gly	Asn	Ser	Gly	Ser	Asn	Leu	Gln	Leu	Ile	Tyr	Asn	Leu	Thr	Leu	Cys	35	40	45	
Glu	Leu	Asn	Gly	Thr	Asp	Trp	Leu	Ala	Asn	Lys	Phe	Asp	Trp	Ala	Val	50	55	60	
Glu	Cys	Phe	Val	Ile	Phe	Pro	Val	Leu	Thr	His	Ile	Val	Ser	Tyr	Gly	65	70	75	80
Ala	Leu	Thr	Thr	Ser	His	Phe	Leu	Asp	Thr	Val	Gly	Leu	Val	Thr	Val	85	90	95	
Ser	Thr	Ala	Gly	Phe	Val	His	Gly	Arg	Tyr	Val	Leu	Ser	Ser	Met	Tyr	100	105	110	
Ala	Val	Cys	Ala	Leu	Ala	Ala	Leu	Ile	Cys	Phe	Val	Ile	Arg	Leu	Ala	115	120	125	
Lys	Asn	Cys	Met	Ser	Trp	Arg	Tyr	Ser	Cys	Thr	Arg	Tyr	Thr	Asn	Phe	130	135	140	
Leu	Leu	Asp	Thr	Lys	Gly	Arg	Leu	Tyr	Arg	Trp	Arg	Ser	Pro	Val	Ile	145	150	155	160
Ile	Glu	Lys	Arg	Gly	Lys	Val	Glu	Val	Glu	Gly	His	Leu	Ile	Asp	Leu	165	170	175	
Lys	Arg	Val	Val	Leu	Asp	Gly	Ser	Ala	Ala	Thr	Pro	Val	Thr	Arg	Val	180	185	190	
Ser	Ala	Glu	Gln	Trp	Ser	Arg	Pro									195	200		

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAG TCG TCC TTA GAT GAC TTC TGT CAT GAT AGC ACG GCT CCA CAA	48
Met Glu Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTC TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT	96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
GTC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC	192
Val Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	
50 55 60	
TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA	240
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC	288
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT	336
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	

GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT	384
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC	432
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	
GGC ACA TTG GTG CCC GGG TTA AAA AGC CTC GTG TTG GGT GGC AGA AAA	480
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	
145 150 155 160	
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA	522
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Glu	Ser	Ser	Leu	Asp	Asp	Phe	Cys	His	Asp	Ser	Thr	Ala	Pro	Gln
1				5					10					15	
Lys	Val	Leu	Leu	Ala	Phe	Ser	Ile	Thr	Tyr	Thr	Pro	Val	Met	Ile	Tyr
			20					25					30		
Ala	Leu	Lys	Val	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu
		35					40					45			
Val	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His
	50					55					60				
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala
65					70					75					80
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr
				85					90					95	
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro
			100					105					110		

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn  
 115 120 125  
 Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn  
 130 135 140  
 Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys  
 145 150 155 160  
 Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CCA AAT AAC ACC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAC	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His	
20 25 30	
CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTC CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	

CAT CAC TTT ACC CCT AGT GAG CGT CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His	
20 25 30	
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG AGA TGT TCT CAC AAA TTG GGG CGT TTC TTG ACT CCG CAC TCT TGC	48
Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys	
1 5 10 15	
TTC TGG TGG CTT TTT TTG CTG TGT ACC GGC TTG TCC TGG TCC TTT GCC	96
Phe Trp Trp Leu Phe Leu Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala	
20 25 30	
GAT GGC AAC GGC GAC AGC TCG ACA TAC CAA TAC ATA TAT AAC TTG ACG	144
Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr	
35 40 45	
ATA TGC GAG CTG AAT GGG ACC GAC TGG TTG TCC AGC CAT TTT GGT TGG	192
Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp	
50 55 60	
GCA GTC GAG ACC TTT GTG CTT TAC CCG GTT GCC ACT CAT ATC CTC TCA	240
Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser	
65 70 75 80	
CTG GGT TTT CTC ACA ACA AGC CAT TTT TTT GAC GCG CTC GGT CTC GGC	288
Leu Gly Phe Leu Thr Thr Ser His Phe Phe Asp Ala Leu Gly Leu Gly	
85 90 95	
GCT GTA TCC ACT GCA GGA TTT GTT GGC GGG CGG TAC GTA CTC TGC AGC	336
Ala Val Ser Thr Ala Gly Phe Val Gly Gly Arg Tyr Val Leu Cys Ser	
100 105 110	

GTC TAC GGC GCT TGT GCT TTC GCA GCG TTC GTA TGT TTT GTC ATC CGT	384
Val Tyr Gly Ala Cys Ala Phe Ala Ala Phe Val Cys Phe Val Ile Arg	
115 120 125	
GCT GCT AAA AAT TGC ATG GCC TGC CGC TAT GCC CGT ACC CGG TTT ACC	432
Ala Ala Lys Asn Cys Met Ala Cys Arg Tyr Ala Arg Thr Arg Phe Thr	
130 135 140	
AAC TTC ATT GTG GAC GAC CGG GGG AGA GTT CAT CGA TGG AAG TCT CCA	480
Asn Phe Ile Val Asp Asp Arg Gly Arg Val His Arg Trp Lys Ser Pro	
145 150 155 160	
ATA GTG GTA GAA AAA TTG GGC AAA GCC GAA GTC GAT GGC AAC CTC GTC	528
Ile Val Val Glu Lys Leu Gly Lys Ala Glu Val Asp Gly Asn Leu Val	
165 170 175	
ACC ATC AAA CAT GTC GTC CTC GAA GGG GTT AAA GCT CAA CCC TTG ACG	576
Thr Ile Lys His Val Val Leu Glu Gly Val Lys Ala Gln Pro Leu Thr	
180 185 190	
AGG ACT TCG GCT GAG CAA TGG GAG GCC TAG	606
Arg Thr Ser Ala Glu Gln Trp Glu Ala	
195 200	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys
1 5 10 15
Phe Trp Trp Leu Phe Leu Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala
20 25 30
Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr
35 40 45
Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp
50 55 60
Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser
65 70 75 80

Leu	Gly	Phe	Leu	Thr	Thr	Ser	His	Phe	Phe	Asp	Ala	Leu	Gly	Leu	Gly	
				85					90					95		
Ala	Val	Ser	Thr	Ala	Gly	Phe	Val	Gly	Gly	Arg	Tyr	Val	Leu	Cys	Ser	
			100					105					110			
Val	Tyr	Gly	Ala	Cys	Ala	Phe	Ala	Ala	Phe	Val	Cys	Phe	Val	Ile	Arg	
		115					120					125				
Ala	Ala	Lys	Asn	Cys	Met	Ala	Cys	Arg	Tyr	Ala	Arg	Thr	Arg	Phe	Thr	
		130				135					140					
Asn	Phe	Ile	Val	Asp	Asp	Arg	Gly	Arg	Val	His	Arg	Trp	Lys	Ser	Pro	
145					150					155					160	
Ile	Val	Val	Glu	Lys	Leu	Gly	Lys	Ala	Glu	Val	Asp	Gly	Asn	Leu	Val	
				165					170					175		
Thr	Ile	Lys	His	Val	Val	Leu	Glu	Gly	Val	Lys	Ala	Gln	Pro	Leu	Thr	
			180					185					190			
Arg	Thr	Ser	Ala	Glu	Gln	Trp	Glu	Ala								
		195					200									

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGGCTGGCA TTCTTGAGGC ATCCAGTGT TTGAATTGGA AGAATGCGTG GTGAATGGCA	60
CTGATTGACA TTGTGCCTCT AAGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTAAGA	120
TTTAATTGGC GAGAACCACA CGGCCGAAAT TAAAAAAAAA AAAA	164



(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG GGA GGC CTA GAC GAT TTT TGC AAC GAT CCT ATC GCC GCA CAA AAG	48
Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys	
1 5 10 15	
CTC GTG CTA GCC TTT AGC ATC ACA TAC ACA CCT ATA ATG ATA TAC GCC	96
Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala	
20 25 30	
CTT AAG GTG TCA CGC GGC CGA CTC CTG GGG CTG TTG CAC ATC CTA ATA	144
Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile	
35 40 45	
TTT CTG AAC TGT TCC TTT ACA TTC GGA TAC ATG ACA TAT GTG CAT TTT	192
Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe	
50 55 60	
CAA TCC ACC AAC CGT GTC GCA CTT ACC CTG GGG GCT GTT GTC GCC CTT	240
Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu	
65 70 75 80	
CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC	288
Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	
85 90 95	
AGA TGC AGA TTG TGT TGC CTT GGC CGG CGA TAC ATT CTG GCC CCT GCC	336
Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala	
100 105 110	

CAT CAC GTA GAA AGT GCT GCA GGT CTC CAT TCA ATC TCA GCG TCT GGT	384
His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly	
115 120 125	
AAC CGA GCA TAC GCT GTG AGA AAG CCC GGA CTA ACA TCA GTG AAC GGC	432
Asn Arg Ala Tyr Ala Val Arg Lys Pro Gly Leu Thr Ser Val Asn Gly	
130 135 140	
ACT CTA GTA CCA GGA CTT CGG AGC CTC GTG CTG GGC GGC AAA CGA GCT	480
Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Arg Ala	
145 150 155 160	
GTT AAA CGA GGA GTG GTT AAC CTC GTC AAG TAT GGC CGG TAA	522
Val Lys Arg Gly Val Val Asn Leu Val Lys Tyr Gly Arg	
165 170	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys	
1 5 10 15	
Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala	
20 25 30	
Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile	
35 40 45	
Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe	
50 55 60	
Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu	
65 70 75 80	
Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	
85 90 95	
Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala	
100 105 110	
His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly	
115 120 125	

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Asn Arg Ala Tyr Ala Val Arg Lys Pro Gly Leu Thr Ser Val Asn Gly
130                      135                      140

Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Arg Ala
145                      150                      155                      160

Val Lys Arg Gly Val Val Asn Leu Val Lys Tyr Gly Arg
165                      170

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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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ATG GCC GGT AAA AAC CAG AGC CAG AAG AAA AAG AAA AGT ACA GCT CCG      48
Met Ala Gly Lys Asn Gln Ser Gln Lys Lys Lys Lys Ser Thr Ala Pro
 1                      5                      10                      15

ATG GGG AAT GGC CAG CCA GTC AAT CAA CTG TGC CAG TTG CTG GGT GCA      96
Met Gly Asn Gly Gln Pro Val Asn Gln Leu Cys Gln Leu Leu Gly Ala
          20                      25                      30

ATG ATA AAG TCC CAG CGC CAG CAA CCT AGG GGA GGA CAG GCC AAA AAG     144
Met Ile Lys Ser Gln Arg Gln Gln Pro Arg Gly Gly Gln Ala Lys Lys
          35                      40                      45

AAA AAG CCT GAG AAG CCA CAT TTT CCC CTG GCT GCT GAA GAT GAC ATC     192
Lys Lys Pro Glu Lys Pro His Phe Pro Leu Ala Ala Glu Asp Asp Ile
          50                      55                      60

CGG CAC CAC CTC ACC CAG ACT GAA CGC TCC CTC TGC TTG CAA TCG ATC     240
Arg His His Leu Thr Gln Thr Glu Arg Ser Leu Cys Leu Gln Ser Ile
 65                      70                      75                      80

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CAG ACG GCT TTC AAT CAA GGC GCA GGA ACT GCG TCG CTT TCA TCC AGC	288
Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser Ser	
85 90 95	
GGG AAG GTC AGT TTT CAG GTT GAG TTT ATG CTG CCG GTT GCT CAT ACA	336
Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr	
100 105 110	
GTG CGC CTG ATT CGC GTG ACT TCT ACA TCC GCC AGT CAG GGT GCA AGT	384
Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser	
115 120 125	
TAA	387

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Gly Lys Asn Gln Ser Gln Lys Lys Lys Lys Ser Thr Ala Pro	
1 5 10 15	
Met Gly Asn Gly Gln Pro Val Asn Gln Leu Cys Gln Leu Leu Gly Ala	
20 25 30	
Met Ile Lys Ser Gln Arg Gln Gln Pro Arg Gly Gly Gln Ala Lys Lys	
35 40 45	
Lys Lys Pro Glu Lys Pro His Phe Pro Leu Ala Ala Glu Asp Asp Ile	
50 55 60	
Arg His His Leu Thr Gln Thr Glu Arg Ser Leu Cys Leu Gln Ser Ile	
65 70 75 80	
Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser Ser	
85 90 95	
Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr	
100 105 110	
Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser	
115 120 125	

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGACAGTC AGGTGAATGG CCGCGATTGG CGTGTGGCCT CTGAGTCACC TATTCAATTA	60
GGGCGATCAC ATGGGGGTCA TACTTAATCA GGCAGGAACC ATGTGACCGA AATTAAAAAA	120
AAAAAAA	127

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGATCCGG TATTGGCAA TGTGTC	26
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(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTGTTTTCC ACGAGAACCG CTTAAGGG

28

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGATCCAG AGTTTCAGCG G

21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGTTAGTCG ACACGGTCTT AAGGG

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGATCCTT GTTAAATATG CC

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTTACGCACC ACTTAAGGG

19

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AATGGGGCTT CTCCGG

16

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 886 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGAGTCGT CCTTAGATGA CTTCTGTCAT GATAGCACGG CTCCACAAAA GGTGCTCTTG	60
GCGTTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGGTCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTAAAAAGCC TCGTGTTGGG TGGCAGAAAA	480
GCTGTTAAAC AGGGAGTGGT AAACCTTGTT AAATATGCCA AATAACACCG GCAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCTCAC CAAAACCACT CCAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTCC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC	720
TAGTGAGCGT CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCTACGCA	840
TCATACTGTG CGCCTGATCC GCGTCACAGC ATCACCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGGGTCGT CCTTAGATGA CTTCTGCCAT GATAGTACGG CTCCACAAAA GGTGCTTTTG	60
GCGTTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA	480
GCTGTAAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GCAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCTCAG CAAAACCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAACA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCCC	720
TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCAACGCA	840
TCATACTGTG CGCTTGATCC GCGTCACAGC ATCACCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGGGGTCGT CCTTAGATGA CTTCTGTCAT GACAGCACGG CTCCACAAAA GGTGCTTTTG	60
GCGTTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TGAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCACTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTTCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA	480
GCTGTAAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GTAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGCAAGAT	600
CATCGCTCAG CAAAATCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC	720
TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACTGTG GAGTTTAGTT TGCCTACGCA	840
TCATACTGTG CGCCTGATCC GCGTCACAGC ATCACCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGGGTCGT CCTTAGATGA CTTCTGTTAT GATAGTACGG CTCCACAAAA GGTGCTTTTG	60
GCATTTTCTA TTACCTACAC GCCAGTAATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATTTTC CTGAACTGTG CTTTCACCTT CGGGTACATG	180
ACATTCATGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA	480
GCTGTTAAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GCAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCCCAG CAAAACCACT CTAGAGGCAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC	720
TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAAAGTGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCTACGCA	840
TCATACTGTG CGCTTGATCC GCGTCACAGC ATCACCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGGGGTCGT CCTTAGATGA CTTCTGCCAT GATAGCACGG CTCCACAAAA GGTGCTTTTG	60
GCGTTCTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAAGTAAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTAAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG CACAAACAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTTTG GCCCCTGCCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATAGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTTA ACGGCACATT GGTGCCCCGGG TTGAAAAGCC TCGTGTTGGG TGGCAGAAAA	480
GCTGTCAAAC AGGGAGTGGT AAACCTTGTT AAATATGCCA AATAACAACG GCAAGCAGCA	540
GAAGAAAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCTCAG CAAAACCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAACA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCTC	720
TGGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACAGCC TTTAATCAAG GCGCTGGAAC	780
TTGTACCCTG TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCGACGCA	840
TCATACTGTG CGCTTGATCC GCGTCACAGC GTCACCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGGGTCGT CCCTAGACGA CTTTGTGCAAT GATAGCACGG CTCCACAAAA GGTGCTTTTG	60
GCGTTTTCTA TTACCTACAC GCCGGTGATG ATATATGCTC TAAAGGTAAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATTTTT CTGAATTGTG CTTTTACTTT CGGGTACATG	180
ACATTCGTGC ACTTTGAGAG CACAAATAGG GTCGCGCTCA CTATGGGAGC AGTAGTCGCA	240
CTTCTCTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCCC ACCACGTTGA GAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTTA ACGGCACATT GGTGCCCCGGG TTGAGAAGCC TCGTGTGTTGGG TGGCAAAAAA	480
GCTGTTAAGC AGGGAGTGGT AAACCTTGTT AAATATGCCA AATAACAACG GCAAGCAGCA	540
GAAGAAAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTC TGCCAAATGC TGGGTAAGAT	600
CATCGCCCAG CAAAACCACT CCAGAGGTAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCCC	720
CAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACTGCC TTTAATCAGG GCGCTGGGAC	780
CTGTATCCTA TCAGATTCAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCGACGCA	840
TCATACTGTG CGCCTGATTC GCGTCACGGC ACCACCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGGAGGCC TAGACGATTT TTGCAACGAT CCTATCGCCG CACAAAAGCT CGTGCTAGCC	60
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TTTAGCATCA CATAACACC TATAATGATA TACGCCCTTA AGGTGTCACG CGGCCGACTC	120
CTGGGGCTGT TGCACATCCT AATATTTCTG AACTGTTCTT TTACATTCGG ATACATGACA	180
TATGTGCATT TTCAATCCAC CAACCGTGTC GCACTTACCC TGGGGGCTGT TGTCGCCCTT	240
CTGTGGGGTG TTTACAGCTT CACAGAGTCA TGGAAGTTTA TCACTTCCAG ATGCAGATTG	300
TGTTGCCTTG GCCGGCGATA CATTCTGGCC CCTGCCCATC ACGTAGAAAG TGCTGCAGGT	360
CTCCATTCAA TCTCAGCGTC TGGTAACCGA GCATACGCTG TGAGAAAGCC CGGACTAACA	420
TCAGTGAACG GCACTCTAGT ACCAGGACTT CGGAGCCTCG TGCTGGGCGG CAAACGAGCT	480
GTTAAACGAG GAGTGGTTAA CCTCGTCAAG TATGGCCGGT AAAAACCAGA GCCAGAAGAA	540
AAAGAAAAGT ACAGCTCCGA TGGGGAATGG CCAGCCAGTC AATCAACTGT GCCAGTTGCT	600
GGGTGCAATG ATAAAGTCCC AGCGCCAGCA ACCTAGGGGA GGACAGGCCA AAAAGAAAAA	660
GCCTGAGAAG CCACATTTTC CCCTGGCTGC TGAAGATGAC ATCCGGCACC ACCTCACCCA	720
GACTGAACGC TCCCTCTGCT TGCAATCGAT CCAGACGGCT TTCAATCAAG GCGCAGGAAC	780
TGCGTCGCTT TCATCCAGCG GGAAGGTCAG TTTTCAGGTT GAGTTTATGC TGCCGGTTGC	840
TCATACAGTG CGCCTGATTC GCGTGACTTC TACATCCGCC AGTCAGGGTG CAAGTTAA	898

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG GGG TCG TCC TTA GAT GAC TTC TGC CAT GAT AGT ACG GCT CCA CAA	48
Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT	96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
ATC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC	192
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	
50 55 60	
TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA	240
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC	288
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT	336
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	
GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT	384
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC	432
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	
GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA	480
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	
145 150 155 160	
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA	522
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met 1	Gly	Ser	Ser	Leu 5	Asp	Asp	Phe	Cys	His 10	Asp	Ser	Thr	Ala	Pro 15	Gln
Lys	Val	Leu	Leu 20	Ala	Phe	Ser	Ile	Thr 25	Tyr	Thr	Pro	Val	Met 30	Ile	Tyr
Ala	Leu	Lys 35	Val	Ser	Arg	Gly	Arg 40	Leu	Leu	Gly	Leu	Leu 45	His	Leu	Leu
Ile	Phe 50	Leu	Asn	Cys	Ala	Phe 55	Thr	Phe	Gly	Tyr	Met 60	Thr	Phe	Val	His
Phe 65	Gln	Ser	Thr	Asn	Lys 70	Val	Ala	Leu	Thr	Met 75	Gly	Ala	Val	Val	Ala 80
Leu	Leu	Trp	Gly	Val 85	Tyr	Ser	Ala	Ile	Glu 90	Thr	Trp	Lys	Phe	Ile 95	Thr
Ser	Arg	Cys	Arg 100	Leu	Cys	Leu	Leu	Gly 105	Arg	Lys	Tyr	Ile	Leu 110	Ala	Pro
Ala	His	His 115	Val	Glu	Ser	Ala	Ala 120	Gly	Phe	His	Pro	Ile 125	Ala	Ala	Asn
Asp	Asn 130	His	Ala	Phe	Val	Val 135	Arg	Arg	Pro	Gly	Ser 140	Thr	Thr	Val	Asn
Gly 145	Thr	Leu	Val	Pro	Gly 150	Leu	Lys	Ser	Leu	Val 155	Leu	Gly	Gly	Arg	Lys 160
Ala	Val	Lys	Gln	Gly 165	Val	Val	Asn	Leu	Val 170	Lys	Tyr	Ala	Lys		

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATG GGG TCG TCC TTA GAT GAC TTC TGT CAT GAC AGC ACG GCT CCA CAA	48
Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT	96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCC CTG AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
ATC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC	192
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	
50 55 60	
TTT CAG AGT ACA AAT AAG GTC GCA CTC ACT ATG GGA GCA GTA GTT GCA	240
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC	288
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT	336
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	
GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT	384
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
GAT AAC CAC GCA TTT GTC GTT CGG CGT CCC GGC TCC ACT ACG GTC AAC	432
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	

GGC	ACA	TTG	GTG	CCC	GGG	TTG	AAA	AGC	CTC	GTG	TTG	GGT	GGC	AGA	AAA	480
Gly	Thr	Leu	Val	Pro	Gly	Leu	Lys	Ser	Leu	Val	Leu	Gly	Gly	Arg	Lys	
145					150					155					160	

GCT	GTT	AAA	CAG	GGA	GTG	GTA	AAC	CTT	GTC	AAA	TAT	GCC	AAA			522
Ala	Val	Lys	Gln	Gly	Val	Val	Asn	Leu	Val	Lys	Tyr	Ala	Lys			
				165					170							

TAA																525
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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Gly	Ser	Ser	Leu	Asp	Asp	Phe	Cys	His	Asp	Ser	Thr	Ala	Pro	Gln	
1				5					10					15		
Lys	Val	Leu	Leu	Ala	Phe	Ser	Ile	Thr	Tyr	Thr	Pro	Val	Met	Ile	Tyr	
			20					25					30			
Ala	Leu	Lys	Val	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu	
		35					40					45				
Ile	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His	
	50					55					60					
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala	
65					70					75					80	
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr	
				85					90					95		
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro	
			100					105					110			
Ala	His	His	Val	Glu	Ser	Ala	Ala	Gly	Phe	His	Pro	Ile	Ala	Ala	Asn	
		115					120					125				
Asp	Asn	His	Ala	Phe	Val	Val	Arg	Arg	Pro	Gly	Ser	Thr	Thr	Val	Asn	
	130					135					140					
Gly	Thr	Leu	Val	Pro	Gly	Leu	Lys	Ser	Leu	Val	Leu	Gly	Gly	Arg	Lys	
145					150					155					160	

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATG GGG TCG TCC TTA GAT GAC TTC TGT TAT GAT AGT ACG GCT CCA CAA	48
Met Gly Ser Ser Leu Asp Asp Phe Cys Tyr Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTT TTG GCA TTT TCT ATT ACC TAC ACG CCA GTA ATG ATA TAT	96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
ATT TTC CTG AAC TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC ATG CAC	192
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Met His	
50 55 60	
TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA	240
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC	288
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	

TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT	336
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	
GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT	384
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC	432
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	
GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA	480
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	
145 150 155 160	
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA	522
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Ser Ser Leu Asp Asp Phe Cys Tyr Asp Ser Thr Ala Pro Gln	
1 5 10 15	
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Met His	
50 55 60	
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro  
100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn  
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn  
130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys  
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG GGG TCG TCC TTA GAT GAC TTC TGC CAT GAT AGC ACG GCT CCA CAA	48
Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTT TTG GCG TTC TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT	96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCC CTA AAA GTA AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	

ATC	TTC	CTA	AAT	TGT	GCT	TTC	ACC	TTC	GGG	TAC	ATG	ACA	TTC	GTG	CAC	192
Ile	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His	
	50					55					60					
TTT	CAG	AGC	ACA	AAC	AAG	GTC	GCG	CTC	ACT	ATG	GGA	GCA	GTA	GTT	GCA	240
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala	
	65				70					75					80	
CTC	CTT	TGG	GGG	GTG	TAC	TCA	GCC	ATA	GAA	ACC	TGG	AAA	TTC	ATC	ACC	288
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr	
				85					90					95		
TCC	AGA	TGC	CGT	TTG	TGC	TTG	CTA	GGC	CGC	AAG	TAC	ATT	TTG	GCC	CCT	336
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro	
			100					105					110			
GCC	CAC	CAC	GTT	GAA	AGT	GCC	GCA	GGC	TTT	CAT	CCG	ATA	GCG	GCA	AAT	384
Ala	His	His	Val	Glu	Ser	Ala	Ala	Gly	Phe	His	Pro	Ile	Ala	Ala	Asn	
			115				120					125				
GAT	AAC	CAC	GCA	TTT	GTC	GTC	CGG	CGT	CCC	GGC	TCC	ACT	ACG	GTT	AAC	432
Asp	Asn	His	Ala	Phe	Val	Val	Arg	Arg	Pro	Gly	Ser	Thr	Thr	Val	Asn	
	130					135					140					
GGC	ACA	TTG	GTG	CCC	GGG	TTG	AAA	AGC	CTC	GTG	TTG	GGT	GGC	AGA	AAA	480
Gly	Thr	Leu	Val	Pro	Gly	Leu	Lys	Ser	Leu	Val	Leu	Gly	Gly	Arg	Lys	
	145				150					155					160	
GCT	GTC	AAA	CAG	GGA	GTG	GTA	AAC	CTT	GTT	AAA	TAT	GCC	AAA			522
Ala	Val	Lys	Gln	Gly	Val	Val	Asn	Leu	Val	Lys	Tyr	Ala	Lys			
				165					170							
TAA																525

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Gly	Ser	Ser	Leu	Asp	Asp	Phe	Cys	His	Asp	Ser	Thr	Ala	Pro	Gln	
1				5					10					15		
Lys	Val	Leu	Leu	Ala	Phe	Ser	Ile	Thr	Tyr	Thr	Pro	Val	Met	Ile	Tyr	
			20					25					30			

Ala	Leu	Lys	Val	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu
		35					40					45			
Ile	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His
	50					55					60				
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala
65					70					75					80
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr
				85					90					95	
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro
			100					105					110		
Ala	His	His	Val	Glu	Ser	Ala	Ala	Gly	Phe	His	Pro	Ile	Ala	Ala	Asn
		115					120					125			
Asp	Asn	His	Ala	Phe	Val	Val	Arg	Arg	Pro	Gly	Ser	Thr	Thr	Val	Asn
	130					135					140				
Gly	Thr	Leu	Val	Pro	Gly	Leu	Lys	Ser	Leu	Val	Leu	Gly	Gly	Arg	Lys
145					150					155					160
Ala	Val	Lys	Gln	Gly	Val	Val	Asn	Leu	Val	Lys	Tyr	Ala	Lys		
				165					170						

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG GGG TCG TCC CTA GAC GAC TTT TGC AAT GAT AGC ACG GCT CCA CAA	48
Met Gly Ser Ser Leu Asp Asp Phe Cys Asn Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCG GTG ATG ATA TAT	96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCT CTA AAG GTA AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
ATT TTT CTG AAT TGT GCT TTT ACT TTC GGG TAC ATG ACA TTC GTG CAC	192
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	
50 55 60	
TTT GAG AGC ACA AAT AGG GTC GCG CTC ACT ATG GGA GCA GTA GTC GCA	240
Phe Glu Ser Thr Asn Arg Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
CTT CTC TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC	288
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT	336
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	
GCC CAC CAC GTT GAG AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT	384
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTT AAC	432
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	
GGC ACA TTG GTG CCC GGG TTG AGA AGC CTC GTG TTG GGT GGC AAA AAA	480
Gly Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Lys	
145 150 155 160	
GCT GTT AAG CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA	522
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
165 170	
TAA	525



(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 174 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Gly	Ser	Ser	Leu	Asp	Asp	Phe	Cys	Asn	Asp	Ser	Thr	Ala	Pro	Gln	
1				5					10					15		
Lys	Val	Leu	Leu	Ala	Phe	Ser	Ile	Thr	Tyr	Thr	Pro	Val	Met	Ile	Tyr	
		20						25					30			
Ala	Leu	Lys	Val	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu	
		35					40					45				
Ile	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His	
	50					55					60					
Phe	Glu	Ser	Thr	Asn	Arg	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala	
65					70					75					80	
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr	
				85					90					95		
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro	
			100					105					110			
Ala	His	His	Val	Glu	Ser	Ala	Ala	Gly	Phe	His	Pro	Ile	Ala	Ala	Asn	
		115					120					125				
Asp	Asn	His	Ala	Phe	Val	Val	Arg	Arg	Pro	Gly	Ser	Thr	Thr	Val	Asn	
	130						135				140					
Gly	Thr	Leu	Val	Pro	Gly	Leu	Arg	Ser	Leu	Val	Leu	Gly	Gly	Lys	Lys	
145					150					155					160	
Ala	Val	Lys	Gln	Gly	Val	Val	Asn	Leu	Val	Lys	Tyr	Ala	Lys			
				165					170							

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 372 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAC AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
CAT CAC TTC ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCA ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC TTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met	Pro	Asn	Asn	Asn	Gly	Lys	Gln	Gln	Lys	Arg	Lys	Lys	Gly	Asp	Gly	
1				5					10					15		
Gln	Pro	Val	Asn	Gln	Leu	Cys	Gln	Met	Leu	Gly	Lys	Ile	Ile	Ala	Gln	
			20					25					30			
Gln	Asn	Gln	Ser	Arg	Gly	Lys	Gly	Pro	Gly	Lys	Lys	Asn	Lys	Lys	Lys	
		35					40					45				
Asn	Pro	Glu	Lys	Pro	His	Phe	Pro	Leu	Ala	Thr	Glu	Asp	Asp	Val	Arg	
	50					55					60					
His	His	Phe	Thr	Pro	Ser	Glu	Arg	Gln	Leu	Cys	Leu	Ser	Ser	Ile	Gln	
65					70					75				80		
Thr	Ala	Phe	Asn	Gln	Gly	Ala	Gly	Thr	Cys	Thr	Leu	Ser	Asp	Ser	Gly	
			85						90					95		
Arg	Ile	Ser	Tyr	Thr	Val	Glu	Phe	Ser	Leu	Pro	Thr	His	His	Thr	Val	
		100						105					110			
Arg	Leu	Ile	Arg	Val	Thr	Ala	Ser	Pro	Ser	Ala						
	115						120									

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG CCA AAT AAC AAC GGT AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGC AAG ATC ATC GCT CAG	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
CAA AAT CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
CAT CAC TTT ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Pro	Asn	Asn	Asn	Gly	Lys	Gln	Gln	Lys	Arg	Lys	Lys	Gly	Asp	Gly	
1				5					10					15		
Gln	Pro	Val	Asn	Gln	Leu	Cys	Gln	Met	Leu	Gly	Lys	Ile	Ile	Ala	Gln	
			20					25					30			
Gln	Asn	Gln	Ser	Arg	Gly	Lys	Gly	Pro	Gly	Lys	Lys	Asn	Lys	Lys	Lys	
		35					40					45				
Asn	Pro	Glu	Lys	Pro	His	Phe	Pro	Leu	Ala	Thr	Glu	Asp	Asp	Val	Arg	
	50					55					60					
His	His	Phe	Thr	Pro	Ser	Glu	Arg	Gln	Leu	Cys	Leu	Ser	Ser	Ile	Gln	
65					70					75					80	
Thr	Ala	Phe	Asn	Gln	Gly	Ala	Gly	Thr	Cys	Thr	Leu	Ser	Asp	Ser	Gly	
			85						90					95		
Arg	Ile	Ser	Tyr	Thr	Val	Glu	Phe	Ser	Leu	Pro	Thr	His	His	Thr	Val	
			100					105					110			
Arg	Leu	Ile	Arg	Val	Thr	Ala	Ser	Pro	Ser	Ala						
		115					120									

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATG	CCA	AAT	AAC	AAC	GGC	AAG	CAG	CAG	AAG	AGA	AAG	AAG	GGG	GAT	GGC	48
Met	Pro	Asn	Asn	Asn	Gly	Lys	Gln	Gln	Lys	Arg	Lys	Lys	Gly	Asp	Gly	
1				5					10					15		
CAG	CCA	GTC	AAT	CAG	CTG	TGC	CAG	ATG	CTG	GGT	AAG	ATC	ATC	GCC	CAG	96
Gln	Pro	Val	Asn	Gln	Leu	Cys	Gln	Met	Leu	Gly	Lys	Ile	Ile	Ala	Gln	
			20					25					30			
CAA	AAC	CAG	TCT	AGA	GGC	AAG	GGA	CCG	GGA	AAG	AAA	AAT	AAG	AAG	AAA	144
Gln	Asn	Gln	Ser	Arg	Gly	Lys	Gly	Pro	Gly	Lys	Lys	Asn	Lys	Lys	Lys	
		35					40					45				
AAC	CCG	GAG	AAG	CCC	CAT	TTT	CCT	CTA	GCG	ACT	GAA	GAT	GAT	GTC	AGA	192
Asn	Pro	Glu	Lys	Pro	His	Phe	Pro	Leu	Ala	Thr	Glu	Asp	Asp	Val	Arg	
	50					55					60					
CAT	CAC	TTT	ACC	CCT	AGT	GAG	CGG	CAA	TTG	TGT	CTG	TCG	TCA	ATC	CAA	240
His	His	Phe	Thr	Pro	Ser	Glu	Arg	Gln	Leu	Cys	Leu	Ser	Ser	Ile	Gln	
65					70				75					80		
ACT	GCC	TTT	AAT	CAA	GGC	GCT	GGG	ACT	TGC	ACC	CTG	TCA	GAT	TCA	GGG	288
Thr	Ala	Phe	Asn	Gln	Gly	Ala	Gly	Thr	Cys	Thr	Leu	Ser	Asp	Ser	Gly	
				85				90					95			
AGG	ATA	AGT	TAC	ACT	GTG	GAG	TTT	AGT	TTG	CCT	ACG	CAT	CAT	ACT	GTG	336
Arg	Ile	Ser	Tyr	Thr	Val	Glu	Phe	Ser	Leu	Pro	Thr	His	His	Thr	Val	
			100					105					110			
CGC	TTG	ATC	CGC	GTC	ACA	GCA	TCA	CCC	TCA	GCA	TGA					372
Arg	Leu	Ile	Arg	Val	Thr	Ala	Ser	Pro	Ser	Ala						
			115				120									

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Pro	Asn	Asn	Asn	Gly	Lys	Gln	Gln	Lys	Arg	Lys	Lys	Gly	Asp	Gly	
1				5					10					15		
Gln	Pro	Val	Asn	Gln	Leu	Cys	Gln	Met	Leu	Gly	Lys	Ile	Ile	Ala	Gln	
			20					25					30			

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys  
 35 40 45  
 Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg  
 50 55 60  
 His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln  
 65 70 75 80  
 Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly  
 85 90 95  
 Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val  
 100 105 110  
 Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala  
 115 120

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AAA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	

CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAC AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
CAT CAC TTC ACC TCT GGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Ser Gly Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACA GCC TTT AAT CAA GGC GCT GGA ACT TGT ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCG ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC TTG ATC CGC GTC ACA GCG TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly	
1 5 10 15	
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
His His Phe Thr Ser Gly Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	



Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly  
85 90 95  
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val  
100 105 110  
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AAA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTC TGC CAA ATG CTG GGT AAG ATC ATC GCC CAG	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
CAA AAC CAG TCC AGA GGT AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	

CAT CAC TTC ACC CCC AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACT GCC TTT AAT CAG GGC GCT GGG ACC TGT ATC CTA TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Ile Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCG ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATT CGC GTC ACG GCA CCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Pro Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly	
1 5 10 15	
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Ile Leu Ser Asp Ser Gly	
85 90 95	
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
Arg Leu Ile Arg Val Thr Ala Pro Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys Lys Ser Thr Ala Pro Met  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Ser Gln Gly  
1

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 240 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;  
(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TCTTCTTGCC TTTTCTATGC TTCTGAGATG AGTGAAAAGG GATTTAAGGT GGTATTTGGC	60
AATGTGTCAG GCATCGTGGC AGTGTGCGTC AACTTCACCA GTTACGTCCA ACATGTCAAG	120
GAATTTACCC AACGTTCTT GGTAGTTGAC CATGTGCGGC TGCTCCATTT CATGACGCCC	180
GAGACCATGA GGTGGGCAAC TGTTTTAGCC TGTCTTTTTA CCATTCTGTT GGCAATTGA	240

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCTGAATTGA GATGAAATGG GGTCTATGCA AAGCCTTTTT GACAAAATTG GCCAACTTTT	60
TGTGGATGCT TTCACGGAGT TCTTGGTGTC CATTGTTGAT ATCATTATAT TTTTGGCCAT	120
TTTGTTTGGC TTCACCATCG CAGGTTGGCT GGTGGTCTTT TGCATCAGAT TGGTTTGCTC	180
CGCGATACTC CGTGCGCGCC CTGCCATTCA CTCTGAGCAA TTACAGAAGA TCCTATGAGG	240
CCTTTCTCTC TCAGTGCCAG GTGGACATTC CCACCTGGGG AACTAAACAT CCTTTGGGGA	300
TGCTTTGGCA CCATAAGGTG TCAACCCTGA TTGATGAAAT GGTGTCGCGT CGAATGTACC	360
GCATCATGGA AAAAGCAGGA CAGGCTGCCT GGAAACAGGT AGTGAGCGAG GCTACGCTGT	420
CTCGCATTAG TAGTTTGGAT GTGGTGGCTC ATTTTCAGCA TCTTGCCGCC ATTGAAGCCG	480
AGACCTGTAA ATATCTGGCC TCTCGGCTGC CCATGCTACA CCACCTGCGC ATGACAGGGT	540
CAAATGTAAC CATAGTGTAT AATAGTACTT TGAATCAGGT GTTTGCTGTT TTCCCAACCC	600
CTGGTTCCCG GCCAAAGCTT CATGATTTCC AGCAATGGCT AATAGCTGTA CATTCCTCTA	660

TATTTTCCTC TGTTGCAGCT TCTTGTA	720
CTC TTTTGTGT GCTGTGGTTG CGGGTTCCAA	
TGCTACGTAC TGTTTTTGGT TTCCGCTGGT	780
TAGGGGCAAT TTTTCTTTTCG AACTCACGGT	
GAATTACACG GTGTGCCCCG CTTGCCTCAC	840
CCGGCAAGCA GCCGCAGAGG CCTACGAACC	
CGGCAGGTCC CTTTGGTGCA GGATAGGGCA	900
TGATCGATGT GGGGAGGACG ATCATGATGA	
ACTAGGGTTT TGGGTGCCGT CTGGCCTCTC	960
CAGCGAAGGC CACTTGACCA GTGCTTACGC	
CTGGTTGGCG TCCCTGTCCT TCAGCTATAC	1020
GGCCCAGTTC CATCCCGAGA TATTCGGGAT	
AGGGAATGTG AGTCGAGTCT ATGTTGACAT	1080
CAAGCACCAA TTCATTGCG CTGTTCATGA	
TGGGCAGAAC ACCACCTTGC CCCACCATGA	1140
CAACATTTC GCGTGCTTC AGACCTATTA	
CCAGCATCAG GTCGACGGGG GCAATTGGTT	1200
TCACCTAGAA TGGGTGCGTC CCTTCTTTTC	
CTCTTGGTTG GTTTTAAATG TCTCTTGGTT	1260
TCTCAGGCGT TCGCCTGCAA GCCATGTTTC	
AGTTCGAGTC TTTCAGACAT CAAGACCAAC	1320
ACCACCGCAG CGGCAGGCTT TGCTGTCCTC	
CAAGACATCA GTTGCCTTAG GCATCGCAAC	1380
TCGGCCTCTG AGGCGATTTCG CAAAGTCCCT	
CAGTGCCGCA CGGCGATAGG GACACCCGTG	1440
TATATCACTG TCACAGCCAA TGTTACCGAT	
GAGAATTATT TGCATTCTC TGATCTTCTC	1500
ATGCTTTCTT CTTGCCTTTT CTATGCTTCT	
GAGATGAGTG AAAAGGGATT TAAGGTGGTA	1560
TTTGGCAATG TGTCAGGCAT CGTGGCAGTG	
TGCGTCAACT TCACCAGTTA CGTCCAACAT	1620
GTCAAGGAAT TTACCCAACG TTCCTTGGTA	
GTTGACCATG TCGGGCTGCT CCATTTCATG	1680
ACGCCCCGAGA CCATGAGGTG GGCAACTGTT	
TTAGCCTGTC TTTTACCAT TCTGTTGGCA	1740
ATTTGAATGT TTAAGTATGT TGGGGAAATG	
CTTGACCGCG GGCTGTTGCT CGCAATTGCT	1799
TTTTTTATGG TGTATCGTGC CGTCTTGTT	

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATG AAA TGG GGT CTA TGC AAA GCC TTT TTG ACA AAA TTG GCC AAC TTT	48
Met Lys Trp Gly Leu Cys Lys Ala Phe Leu Thr Lys Leu Ala Asn Phe	
1 5 10 15	
TTG TGG ATG CTT TCA CGG AGT TCT TGG TGT CCA TTG TTG ATA TCA TTA	96
Leu Trp Met Leu Ser Arg Ser Ser Trp Cys Pro Leu Leu Ile Ser Leu	
20 25 30	
TAT TTT TGG CCA TTT TGT TTG GCT TCA CCA TCG CAG GTT GGC TGG TGG	144
Tyr Phe Trp Pro Phe Cys Leu Ala Ser Pro Ser Gln Val Gly Trp Trp	
35 40 45	
TCT TTT GCA TCA GAT TGG TTT GCT CCG CGA TAC TCC GTG CGC GCC CTG	192
Ser Phe Ala Ser Asp Trp Phe Ala Pro Arg Tyr Ser Val Arg Ala Leu	
50 55 60	
CCA TTC ACT CTG AGC AAT TAC AGA AGA TCC TAT GAG GCC TTT CTC TCT	240
Pro Phe Thr Leu Ser Asn Tyr Arg Arg Ser Tyr Glu Ala Phe Leu Ser	
65 70 75 80	
CAG TGC CAG GTG GAC ATT CCC ACC TGG GGA ACT AAA CAT CCT TTG GGG	288
Gln Cys Gln Val Asp Ile Pro Thr Trp Gly Thr Lys His Pro Leu Gly	
85 90 95	
ATG CTT TGG CAC CAT AAG GTG TCA ACC CTG ATT GAT GAA ATG GTG TCG	336
Met Leu Trp His His Lys Val Ser Thr Leu Ile Asp Glu Met Val Ser	
100 105 110	
CGT CGA ATG TAC CGC ATC ATG GAA AAA GCA GGA CAG GCT GCC TGG AAA	384
Arg Arg Met Tyr Arg Ile Met Glu Lys Ala Gly Gln Ala Ala Trp Lys	
115 120 125	
CAG GTA GTG AGC GAG GCT ACG CTG TCT CGC ATT AGT AGT TTG GAT GTG	432
Gln Val Val Ser Glu Ala Thr Leu Ser Arg Ile Ser Ser Leu Asp Val	
130 135 140	
GTG GCT CAT TTT CAG CAT CTT GCC GCC ATT GAA GCC GAG ACC TGT AAA	480
Val Ala His Phe Gln His Leu Ala Ala Ile Glu Ala Glu Thr Cys Lys	
145 150 155 160	

TAT CTG GCC TCT CGG CTG CCC ATG CTA CAC CAC CTG CGC ATG ACA GGG	528
Tyr Leu Ala Ser Arg Leu Pro Met Leu His His Leu Arg Met Thr Gly	
165 170 175	
TCA AAT GTA ACC ATA GTG TAT AAT AGT ACT TTG AAT CAG GTG TTT GCT	576
Ser Asn Val Thr Ile Val Tyr Asn Ser Thr Leu Asn Gln Val Phe Ala	
180 185 190	
GTT TTC CCA ACC CCT GGT TCC CGG CCA AAG CTT CAT GAT TTC CAG CAA	624
Val Phe Pro Thr Pro Gly Ser Arg Pro Lys Leu His Asp Phe Gln Gln	
195 200 205	
TGG CTA ATA GCT GTA CAT TCC TCT ATA TTT TCC TCT GTT GCA GCT TCT	672
Trp Leu Ile Ala Val His Ser Ser Ile Phe Ser Ser Val Ala Ala Ser	
210 215 220	
TGT ACT CTT TTT GTT GTG CTG TGG TTG CGG GTT CCA ATG CTA CGT ACT	720
Cys Thr Leu Phe Val Val Leu Trp Leu Arg Val Pro Met Leu Arg Thr	
225 230 235 240	
GTT TTT GGT TTC CGC TGG TTA GGG GCA ATT TTT CTT TCG AAC TCA CGG	768
Val Phe Gly Phe Arg Trp Leu Gly Ala Ile Phe Leu Ser Asn Ser Arg	
245 250 255	
TGA	771

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Lys Trp Gly Leu Cys Lys Ala Phe Leu Thr Lys Leu Ala Asn Phe	
1 5 10 15	
Leu Trp Met Leu Ser Arg Ser Ser Trp Cys Pro Leu Leu Ile Ser Leu	
20 25 30	
Tyr Phe Trp Pro Phe Cys Leu Ala Ser Pro Ser Gln Val Gly Trp Trp	
35 40 45	
Ser Phe Ala Ser Asp Trp Phe Ala Pro Arg Tyr Ser Val Arg Ala Leu	
50 55 60	
Pro Phe Thr Leu Ser Asn Tyr Arg Arg Ser Tyr Glu Ala Phe Leu Ser	
65 70 75 80	

Gln	Cys	Gln	Val	Asp	Ile	Pro	Thr	Trp	Gly	Thr	Lys	His	Pro	Leu	Gly	85	90	95
Met	Leu	Trp	His	His	Lys	Val	Ser	Thr	Leu	Ile	Asp	Glu	Met	Val	Ser	100	105	110
Arg	Arg	Met	Tyr	Arg	Ile	Met	Glu	Lys	Ala	Gly	Gln	Ala	Ala	Trp	Lys	115	120	125
Gln	Val	Val	Ser	Glu	Ala	Thr	Leu	Ser	Arg	Ile	Ser	Ser	Leu	Asp	Val	130	135	140
Val	Ala	His	Phe	Gln	His	Leu	Ala	Ala	Ile	Glu	Ala	Glu	Thr	Cys	Lys	145	150	155
Tyr	Leu	Ala	Ser	Arg	Leu	Pro	Met	Leu	His	His	Leu	Arg	Met	Thr	Gly	165	170	175
Ser	Asn	Val	Thr	Ile	Val	Tyr	Asn	Ser	Thr	Leu	Asn	Gln	Val	Phe	Ala	180	185	190
Val	Phe	Pro	Thr	Pro	Gly	Ser	Arg	Pro	Lys	Leu	His	Asp	Phe	Gln	Gln	195	200	205
Trp	Leu	Ile	Ala	Val	His	Ser	Ser	Ile	Phe	Ser	Ser	Val	Ala	Ala	Ser	210	215	220
Cys	Thr	Leu	Phe	Val	Val	Leu	Trp	Leu	Arg	Val	Pro	Met	Leu	Arg	Thr	225	230	235
Val	Phe	Gly	Phe	Arg	Trp	Leu	Gly	Ala	Ile	Phe	Leu	Ser	Asn	Ser	Arg	245	250	255

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS



(B) LOCATION: 1..762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG GCT AAT AGC TGT ACA TTC CTC TAT ATT TTC CTC TGT TGC AGC TTC	48
Met Ala Asn Ser Cys Thr Phe Leu Tyr Ile Phe Leu Cys Cys Ser Phe	
1 5 10 15	
TTG TAC TCT TTT TGT TGT GCT GTG GTT GCG GGT TCC AAT GCT ACG TAC	96
Leu Tyr Ser Phe Cys Cys Ala Val Val Ala Gly Ser Asn Ala Thr Tyr	
20 25 30	
TGT TTT TGG TTT CCG CTG GTT AGG GGC AAT TTT TCT TTC GAA CTC ACG	144
Cys Phe Trp Phe Pro Leu Val Arg Gly Asn Phe Ser Phe Glu Leu Thr	
35 40 45	
GTG AAT TAC ACG GTG TGC CCG CCT TGC CTC ACC CGG CAA GCA GCC GCA	192
Val Asn Tyr Thr Val Cys Pro Pro Cys Leu Thr Arg Gln Ala Ala Ala	
50 55 60	
GAG GCC TAC GAA CCC GGC AGG TCC CTT TGG TGC AGG ATA GGG CAT GAT	240
Glu Ala Tyr Glu Pro Gly Arg Ser Leu Trp Cys Arg Ile Gly His Asp	
65 70 75 80	
CGA TGT GGG GAG GAC GAT CAT GAT GAA CTA GGG TTT GTG GTG CCG TCT	288
Arg Cys Gly Glu Asp Asp His Asp Glu Leu Gly Phe Val Val Pro Ser	
85 90 95	
GGC CTC TCC AGC GAA GGC CAC TTG ACC AGT GCT TAC GCC TGG TTG GCG	336
Gly Leu Ser Ser Glu Gly His Leu Thr Ser Ala Tyr Ala Trp Leu Ala	
100 105 110	
TCC CTG TCC TTC AGC TAT ACG GCC CAG TTC CAT CCC GAG ATA TTC GGG	384
Ser Leu Ser Phe Ser Tyr Thr Ala Gln Phe His Pro Glu Ile Phe Gly	
115 120 125	
ATA GGG AAT GTG AGT CGA GTC TAT GTT GAC ATC AAG CAC CAA TTC ATT	432
Ile Gly Asn Val Ser Arg Val Tyr Val Asp Ile Lys His Gln Phe Ile	
130 135 140	
TGC GCT GTT CAT GAT GGG CAG AAC ACC ACC TTG CCC CAC CAT GAC AAC	480
Cys Ala Val His Asp Gly Gln Asn Thr Thr Leu Pro His His Asp Asn	
145 150 155 160	
ATT TCA GCC GTG CTT CAG ACC TAT TAC CAG CAT CAG GTC GAC GGG GGC	528
Ile Ser Ala Val Leu Gln Thr Tyr Tyr Gln His Gln Val Asp Gly Gly	
165 170 175	
AAT TGG TTT CAC CTA GAA TGG GTG CGT CCC TTC TTT TCC TCT TGG TTG	576
Asn Trp Phe His Leu Glu Trp Val Arg Pro Phe Phe Ser Ser Trp Leu	
180 185 190	

GTT TTA AAT GTC TCT TGG TTT CTC AGG CGT TCG CCT GCA AGC CAT GTT	624
Val Leu Asn Val Ser Trp Phe Leu Arg Arg Ser Pro Ala Ser His Val	
195 200 205	
TCA GTT CGA GTC TTT CAG ACA TCA AGA CCA ACA CCA CCG CAG CGG CAG	672
Ser Val Arg Val Phe Gln Thr Ser Arg Pro Thr Pro Pro Gln Arg Gln	
210 215 220	
GCT TTG CTG TCC TCC AAG ACA TCA GTT GCC TTA GGC ATC GCA ACT CGG	720
Ala Leu Leu Ser Ser Lys Thr Ser Val Ala Leu Gly Ile Ala Thr Arg	
225 230 235 240	
CCT CTG AGG CGA TTC GCA AAG TCC CTC AGT GCC GCA CGG CGA	762
Pro Leu Arg Arg Phe Ala Lys Ser Leu Ser Ala Ala Arg Arg	
245 250	
TAG	765

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ala	Asn	Ser	Cys	Thr	Phe	Leu	Tyr	Ile	Phe	Leu	Cys	Cys	Ser	Phe	1	5	10	15
Leu	Tyr	Ser	Phe	Cys	Cys	Ala	Val	Val	Ala	Gly	Ser	Asn	Ala	Thr	Tyr	20	25	30	
Cys	Phe	Trp	Phe	Pro	Leu	Val	Arg	Gly	Asn	Phe	Ser	Phe	Glu	Leu	Thr	35	40	45	
Val	Asn	Tyr	Thr	Val	Cys	Pro	Pro	Cys	Leu	Thr	Arg	Gln	Ala	Ala	Ala	50	55	60	
Glu	Ala	Tyr	Glu	Pro	Gly	Arg	Ser	Leu	Trp	Cys	Arg	Ile	Gly	His	Asp	65	70	75	80
Arg	Cys	Gly	Glu	Asp	Asp	His	Asp	Glu	Leu	Gly	Phe	Val	Val	Pro	Ser	85	90	95	
Gly	Leu	Ser	Ser	Glu	Gly	His	Leu	Thr	Ser	Ala	Tyr	Ala	Trp	Leu	Ala	100	105	110	

Ser	Leu	Ser	Phe	Ser	Tyr	Thr	Ala	Gln	Phe	His	Pro	Glu	Ile	Phe	Gly
		115					120					125			
Ile	Gly	Asn	Val	Ser	Arg	Val	Tyr	Val	Asp	Ile	Lys	His	Gln	Phe	Ile
	130					135					140				
Cys	Ala	Val	His	Asp	Gly	Gln	Asn	Thr	Thr	Leu	Pro	His	His	Asp	Asn
145					150					155					160
Ile	Ser	Ala	Val	Leu	Gln	Thr	Tyr	Tyr	Gln	His	Gln	Val	Asp	Gly	Gly
				165					170					175	
Asn	Trp	Phe	His	Leu	Glu	Trp	Val	Arg	Pro	Phe	Phe	Ser	Ser	Trp	Leu
			180					185					190		
Val	Leu	Asn	Val	Ser	Trp	Phe	Leu	Arg	Arg	Ser	Pro	Ala	Ser	His	Val
		195					200					205			
Ser	Val	Arg	Val	Phe	Gln	Thr	Ser	Arg	Pro	Thr	Pro	Pro	Gln	Arg	Gln
	210					215					220				
Ala	Leu	Leu	Ser	Ser	Lys	Thr	Ser	Val	Ala	Leu	Gly	Ile	Ala	Thr	Arg
225					230					235					240
Pro	Leu	Arg	Arg	Phe	Ala	Lys	Ser	Leu	Ser	Ala	Ala	Arg	Arg		
				245					250						

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATG GGT GCG TCC CTT CTT TTC CTC TTG GTT GGT TTT AAA TGT CTC TTG	48
Met Gly Ala Ser Leu Leu Phe Leu Leu Val Gly Phe Lys Cys Leu Leu	
1 5 10 15	
GTT TCT CAG GCG TTC GCC TGC AAG CCA TGT TTC AGT TCG AGT CTT TCA	96
Val Ser Gln Ala Phe Ala Cys Lys Pro Cys Phe Ser Ser Ser Leu Ser	
20 25 30	
GAC ATC AAG ACC AAC ACC ACC GCA GCG GCA GGC TTT GCT GTC CTC CAA	144
Asp Ile Lys Thr Asn Thr Thr Ala Ala Ala Gly Phe Ala Val Leu Gln	
35 40 45	
GAC ATC AGT TGC CTT AGG CAT CGC AAC TCG GCC TCT GAG GCG ATT CGC	192
Asp Ile Ser Cys Leu Arg His Arg Asn Ser Ala Ser Glu Ala Ile Arg	
50 55 60	
AAA GTC CCT CAG TGC CGC ACG GCG ATA GGG ACA CCC GTG TAT ATC ACT	240
Lys Val Pro Gln Cys Arg Thr Ala Ile Gly Thr Pro Val Tyr Ile Thr	
65 70 75 80	
GTC ACA GCC AAT GTT ACC GAT GAG AAT TAT TTG CAT TCC TCT GAT CTT	288
Val Thr Ala Asn Val Thr Asp Glu Asn Tyr Leu His Ser Ser Asp Leu	
85 90 95	
CTC ATG CTT TCT TCT TGC CTT TTC TAT GCT TCT GAG ATG AGT GAA AAG	336
Leu Met Leu Ser Ser Cys Leu Phe Tyr Ala Ser Glu Met Ser Glu Lys	
100 105 110	
GGA TTT AAG GTG GTA TTT GGC AAT GTG TCA GGC ATC GTG GCA GTG TGC	384
Gly Phe Lys Val Val Phe Gly Asn Val Ser Gly Ile Val Ala Val Cys	
115 120 125	
GTC AAC TTC ACC AGT TAC GTC CAA CAT GTC AAG GAA TTT ACC CAA CGT	432
Val Asn Phe Thr Ser Tyr Val Gln His Val Lys Glu Phe Thr Gln Arg	
130 135 140	
TCC TTG GTA GTT GAC CAT GTG CGG CTG CTC CAT TTC ATG ACG CCC GAG	480
Ser Leu Val Val Asp His Val Arg Leu Leu His Phe Met Thr Pro Glu	
145 150 155 160	
ACC ATG AGG TGG GCA ACT GTT TTA GCC TGT CTT TTT ACC ATT CTG TTG	528
Thr Met Arg Trp Ala Thr Val Leu Ala Cys Leu Phe Thr Ile Leu Leu	
165 170 175	
GCA ATT TGA	537
Ala Ile	

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

[illegible]

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus

(C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATG CAA TGG GGT CAC TGT GGA GTA AAA TCA GCC AGC TGT TCG TGG ACG	48
Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr	
1 5 10 15	
CCT TCA CTG AGT TCC TTG TTA GTG TGG TTG ATA TTG CCA TTT TCC TTG	96
Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu	
20 25 30	
CCA TAC TGT TTG GGT TCA CCG TCG CAG GAT GGT TAC TGG TCT TTC TTC	144
Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe	
35 40 45	
TCA GAG TGG TTT GCT CCG CGC TTC TCC GTT CGC GCT CTG CCA TTC ACT	192
Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr	
50 55 60	
CTC CCG AAC TAT CGA AGG TCC TAT GAA GGC TTG TTG CCC AAC TGC AGA	240
Leu Pro Asn Tyr Arg Arg Ser Tyr Glu Gly Leu Leu Pro Asn Cys Arg	
65 70 75 80	
CCG GAT GTC CCA CAA TTT GCA GTC AAG CAC CCA TTG GGT ATG TTT TGG	288
Pro Asp Val Pro Gln Phe Ala Val Lys His Pro Leu Gly Met Phe Trp	
85 90 95	
CAC ATG CGA GTT TCC CAC TTG ATT GAT GAG ATG GTC TCT CGT CGC ATT	336
His Met Arg Val Ser His Leu Ile Asp Glu Met Val Ser Arg Arg Ile	
100 105 110	
TAC CAG ACC ATG GAA CAT TCA GGT CAA GCG GCC TGG AAG CAG GTG GTT	384
Tyr Gln Thr Met Glu His Ser Gly Gln Ala Ala Trp Lys Gln Val Val	
115 120 125	
GGT GAG GCC ACT CTC ACG AAG CTG TCA GGG CTC GAT ATA GTT ACT CAT	432
Gly Glu Ala Thr Leu Thr Lys Leu Ser Gly Leu Asp Ile Val Thr His	
130 135 140	

TTC CAA CAC CTG GCC GCA GTG GAG GCG GAT TCT TGC CGC TTT CTC AGC	480
Phe Gln His Leu Ala Ala Val Glu Ala Asp Ser Cys Arg Phe Leu Ser	
145 150 155 160	
TCA CGA CTC GTG ATG CTA AAA AAT CTT GCC GTT GGC AAT GTG AGC CTA	528
Ser Arg Leu Val Met Leu Lys Asn Leu Ala Val Gly Asn Val Ser Leu	
165 170 175	
CAG TAC AAC ACC ACG TTG GAC CGC GTT GAG CTC ATC TTC CCC ACG CCA	576
Gln Tyr Asn Thr Thr Leu Asp Arg Val Glu Leu Ile Phe Pro Thr Pro	
180 185 190	
GGT ACG AGG CCC AAG TTG ACC GAT TTC AGA CAA TGG CTC ATC AGT GTG	624
Gly Thr Arg Pro Lys Leu Thr Asp Phe Arg Gln Trp Leu Ile Ser Val	
195 200 205	
CAC GCT TCC ATT TTT TCC TCT GTG GCT TCA TCT GTT ACC TTG TTC ATA	672
His Ala Ser Ile Phe Ser Ser Val Ala Ser Ser Val Thr Leu Phe Ile	
210 215 220	
GTG CTT TGG CTT CGA ATT CCA GCT CTA CGC TAT GTT TTT GGT TTC CAT	720
Val Leu Trp Leu Arg Ile Pro Ala Leu Arg Tyr Val Phe Gly Phe His	
225 230 235 240	
TGG CCC ACG GCA ACA CAT CAT TCG AGC TGA	750
Trp Pro Thr Ala Thr His His Ser Ser	
245	

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr	
1 5 10 15	
Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu	
20 25 30	
Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe	
35 40 45	
Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr	
50 55 60	

Leu	Pro	Asn	Tyr	Arg	Arg	Ser	Tyr	Glu	Gly	Leu	Leu	Pro	Asn	Cys	Arg	65	70	75	80
Pro	Asp	Val	Pro	Gln	Phe	Ala	Val	Lys	His	Pro	Leu	Gly	Met	Phe	Trp	85	90	95	
His	Met	Arg	Val	Ser	His	Leu	Ile	Asp	Glu	Met	Val	Ser	Arg	Arg	Ile	100	105	110	
Tyr	Gln	Thr	Met	Glu	His	Ser	Gly	Gln	Ala	Ala	Trp	Lys	Gln	Val	Val	115	120	125	
Gly	Glu	Ala	Thr	Leu	Thr	Lys	Leu	Ser	Gly	Leu	Asp	Ile	Val	Thr	His	130	135	140	
Phe	Gln	His	Leu	Ala	Ala	Val	Glu	Ala	Asp	Ser	Cys	Arg	Phe	Leu	Ser	145	150	155	160
Ser	Arg	Leu	Val	Met	Leu	Lys	Asn	Leu	Ala	Val	Gly	Asn	Val	Ser	Leu	165	170	175	
Gln	Tyr	Asn	Thr	Thr	Leu	Asp	Arg	Val	Glu	Leu	Ile	Phe	Pro	Thr	Pro	180	185	190	
Gly	Thr	Arg	Pro	Lys	Leu	Thr	Asp	Phe	Arg	Gln	Trp	Leu	Ile	Ser	Val	195	200	205	
His	Ala	Ser	Ile	Phe	Ser	Ser	Val	Ala	Ser	Ser	Val	Thr	Leu	Phe	Ile	210	215	220	
Val	Leu	Trp	Leu	Arg	Ile	Pro	Ala	Leu	Arg	Tyr	Val	Phe	Gly	Phe	His	225	230	235	240
Trp	Pro	Thr	Ala	Thr	His	His	Ser	Ser								245			

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad



(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATG GCT CAT CAG TGT GCA CGC TTC CAT TTT TTC CTC TGT GGC TTC ATC	48
Met Ala His Gln Cys Ala Arg Phe His Phe Phe Leu Cys Gly Phe Ile	
1 5 10 15	
TGT TAC CTT GTT CAT AGT GCT TTG GCT TCG AAT TCC AGC TCT ACG CTA	96
Cys Tyr Leu Val His Ser Ala Leu Ala Ser Asn Ser Ser Ser Thr Leu	
20 25 30	
TGT TTT TGG TTT CCA TTG GCC CAC GGC AAC ACA TCA TTC GAG CTG ACC	144
Cys Phe Trp Phe Pro Leu Ala His Gly Asn Thr Ser Phe Glu Leu Thr	
35 40 45	
ATC AAC TAC ACC ATA TGC ATG CCC TGT TCT ACC AGT CAA GCG GCT CGC	192
Ile Asn Tyr Thr Ile Cys Met Pro Cys Ser Thr Ser Gln Ala Ala Arg	
50 55 60	
CAA AGG CTC GAG CCC GGT CGT AAC ATG TGG TGC AAA ATA GGG CAT GAC	240
Gln Arg Leu Glu Pro Gly Arg Asn Met Trp Cys Lys Ile Gly His Asp	
65 70 75 80	
AGG TGT GAG GAG CGT GAC CAT GAT GAG TTG TTA ATG TCC ATC CCG TCC	288
Arg Cys Glu Glu Arg Asp His Asp Glu Leu Leu Met Ser Ile Pro Ser	
85 90 95	
GGG TAC GAC AAC CTC AAA CTT GAG GGT TAT TAT GCT TGG CTG GCT TTT	336
Gly Tyr Asp Asn Leu Lys Leu Glu Gly Tyr Tyr Ala Trp Leu Ala Phe	
100 105 110	
TTG TCC TTT TCC TAC GCG GCC CAA TTC CAT CCG GAG TTG TTC GGG ATA	384
Leu Ser Phe Ser Tyr Ala Ala Gln Phe His Pro Glu Leu Phe Gly Ile	
115 120 125	
GGG AAT GTG TCG CGC GTC TTC GTG GAC AAG CGA CAC CAG TTC ATT TGT	432
Gly Asn Val Ser Arg Val Phe Val Asp Lys Arg His Gln Phe Ile Cys	
130 135 140	
GCC GAG CAT GAT GGA CAC AAT TCA ACC GTA TCT ACC GGA CAC AAC ATC	480
Ala Glu His Asp Gly His Asn Ser Thr Val Ser Thr Gly His Asn Ile	
145 150 155 160	
TCC GCA TTA TAT GCG GCA TAT TAC CAC CAC CAA ATA GAC GGG GGC AAT	528
Ser Ala Leu Tyr Ala Ala Tyr Tyr His His Gln Ile Asp Gly Gly Asn	
165 170 175	

TGG TTC CAT TTG GAA TGG CTG CGG CCA CTC TTT TCT TCC TGG CTG GTG	576
Trp Phe His Leu Glu Trp Leu Arg Pro Leu Phe Ser Ser Trp Leu Val	
180 185 190	
CTC AAC ATA TCA TGG TTT CTG AGG CGT TCG CCT GTA AGC CCT GTT TCT	624
Leu Asn Ile Ser Trp Phe Leu Arg Arg Ser Pro Val Ser Pro Val Ser	
195 200 205	
CGA CGC ATC TAT CAG ATA TTG AGA CCA ACA CGA CCG CGG CTG CCG GTT	672
Arg Arg Ile Tyr Gln Ile Leu Arg Pro Thr Arg Pro Arg Leu Pro Val	
210 215 220	
TCA TGG TCC TTC AGG ACA TCA ATT GTT TCC GAC CTC ACG GGG TCT CAG	720
Ser Trp Ser Phe Arg Thr Ser Ile Val Ser Asp Leu Thr Gly Ser Gln	
225 230 235 240	
CAG CGC AAG AGA AAA TTT CCT TCG GAA AGT CGT CCC AAT GTC GTG AAG	768
Gln Arg Lys Arg Lys Phe Pro Ser Glu Ser Arg Pro Asn Val Val Lys	
245 250 255	
CCG TCG GTA CTC CCC AGT ACA TCA CGA TAA	798
Pro Ser Val Leu Pro Ser Thr Ser Arg	
260 265	

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met	Ala	His	Gln	Cys	Ala	Arg	Phe	His	Phe	Phe	Leu	Cys	Gly	Phe	Ile
1				5					10					15	
Cys	Tyr	Leu	Val	His	Ser	Ala	Leu	Ala	Ser	Asn	Ser	Ser	Ser	Thr	Leu
			20					25					30		
Cys	Phe	Trp	Phe	Pro	Leu	Ala	His	Gly	Asn	Thr	Ser	Phe	Glu	Leu	Thr
		35					40					45			
Ile	Asn	Tyr	Thr	Ile	Cys	Met	Pro	Cys	Ser	Thr	Ser	Gln	Ala	Ala	Arg
	50					55					60				
Gln	Arg	Leu	Glu	Pro	Gly	Arg	Asn	Met	Trp	Cys	Lys	Ile	Gly	His	Asp
65					70					75					80

Arg	Cys	Glu	Glu	Arg	Asp	His	Asp	Glu	Leu	Leu	Met	Ser	Ile	Pro	Ser	85	90	95
Gly	Tyr	Asp	Asn	Leu	Lys	Leu	Glu	Gly	Tyr	Tyr	Ala	Trp	Leu	Ala	Phe	100	105	110
Leu	Ser	Phe	Ser	Tyr	Ala	Ala	Gln	Phe	His	Pro	Glu	Leu	Phe	Gly	Ile	115	120	125
Gly	Asn	Val	Ser	Arg	Val	Phe	Val	Asp	Lys	Arg	His	Gln	Phe	Ile	Cys	130	135	140
Ala	Glu	His	Asp	Gly	His	Asn	Ser	Thr	Val	Ser	Thr	Gly	His	Asn	Ile	145	150	155
Ser	Ala	Leu	Tyr	Ala	Ala	Tyr	Tyr	His	His	Gln	Ile	Asp	Gly	Gly	Asn	165	170	175
Trp	Phe	His	Leu	Glu	Trp	Leu	Arg	Pro	Leu	Phe	Ser	Ser	Trp	Leu	Val	180	185	190
Leu	Asn	Ile	Ser	Trp	Phe	Leu	Arg	Arg	Ser	Pro	Val	Ser	Pro	Val	Ser	195	200	205
Arg	Arg	Ile	Tyr	Gln	Ile	Leu	Arg	Pro	Thr	Arg	Pro	Arg	Leu	Pro	Val	210	215	220
Ser	Trp	Ser	Phe	Arg	Thr	Ser	Ile	Val	Ser	Asp	Leu	Thr	Gly	Ser	Gln	225	230	235
Gln	Arg	Lys	Arg	Lys	Phe	Pro	Ser	Glu	Ser	Arg	Pro	Asn	Val	Val	Lys	245	250	255
Pro	Ser	Val	Leu	Pro	Ser	Thr	Ser	Arg								260	265	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GCT GCG GCC ACT CTT TTC TTC CTG GCT GGT GCT CAA CAT ATC ATG	48
Met Ala Ala Ala Thr Leu Phe Phe Leu Ala Gly Ala Gln His Ile Met	
1 5 10 15	
GTT TCT GAG GCG TTC GCC TGT AAG CCC TGT TTC TCG ACG CAT CTA TCA	96
Val Ser Glu Ala Phe Ala Cys Lys Pro Cys Phe Ser Thr His Leu Ser	
20 25 30	
GAT ATT GAG ACC AAC ACG ACC GCG GCT GCC GGT TTC ATG GTC CTT CAG	144
Asp Ile Glu Thr Asn Thr Thr Ala Ala Ala Gly Phe Met Val Leu Gln	
35 40 45	
GAC ATC AAT TGT TTC CGA CCT CAC GGG GTC TCA GCA GCG CAA GAG AAA	192
Asp Ile Asn Cys Phe Arg Pro His Gly Val Ser Ala Ala Gln Glu Lys	
50 55 60	
ATT TCC TTC GGA AAG TCG TCC CAA TGT CGT GAA GCC GTC GGT ACT CCC	240
Ile Ser Phe Gly Lys Ser Ser Gln Cys Arg Glu Ala Val Gly Thr Pro	
65 70 75 80	
CAG TAC ATC ACG ATA ACG GCT AAC GTG ACC GAC GAA TCA TAC TTG TAC	288
Gln Tyr Ile Thr Ile Thr Ala Asn Val Thr Asp Glu Ser Tyr Leu Tyr	
85 90 95	
AAC GCG GAC CTG CTG ATG CTT TCT GCG TGC CTT TTC TAC GCC TCA GAA	336
Asn Ala Asp Leu Leu Met Leu Ser Ala Cys Leu Phe Tyr Ala Ser Glu	
100 105 110	
ATG AGC GAG AAA GGC TTC AAA GTC ATC TTT GGG AAT GTC TCT GGC GTT	384
Met Ser Glu Lys Gly Phe Lys Val Ile Phe Gly Asn Val Ser Gly Val	
115 120 125	
GTT TCT GCT TGT GTC AAT TTC ACA GAT TAT GTG GCC CAT GTG ACC CAA	432
Val Ser Ala Cys Val Asn Phe Thr Asp Tyr Val Ala His Val Thr Gln	
130 135 140	
CAT ACC CAG CAG CAT CAT CTG GTA ATT GAT CAC ATT CGG TTG CTG CAT	480
His Thr Gln Gln His His Leu Val Ile Asp His Ile Arg Leu Leu His	
145 150 155 160	
TTC CTG ACA CCA TCT GCA ATG AGG TGG GCT ACA ACC ATT GCT TGT TTG	528
Phe Leu Thr Pro Ser Ala Met Arg Trp Ala Thr Thr Ile Ala Cys Leu	
165 170 175	
TTC GCC ATT CTC TTG GCA ATA TGA	552
Phe Ala Ile Leu Leu Ala Ile	
180	

